PCT

RAW SEQUENCE LISTING DATE: 04/12/2005
PATENT APPLICATION: **US/10/501,962A** TIME: 13:37:51

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\04122005\J501962A.raw**

<110> APPLICANT: Braun, Klaus
Braun, Isabell
Debus, Jurgen
Pipkorn, Rudiger
Waldeck, Waldemar
<120> TITLE OF INVENTION: CONJUGATE FOR TREATING PROKARYOTIC INFECTIONS
<130> FILE REFERENCE: 4121-170
<140> CURRENT APPLICATION NUMBER: 10/501,962A
<141> CURRENT FILING DATE: 2004-07-19
<150> PRIOR APPLICATION NUMBER: PCT/DE03/00124
<151> PRIOR FILING DATE: 2003-01-17
<150> PRIOR APPLICATION NUMBER: DE 10201862.6
<151> PRIOR FILING DATE: 2002-01-18
<160> NUMBER OF SEQ ID NOS: 31
<170> SOFTWARE: PatentIn version 3.3
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct
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caccgtcacc ctggatgctg taggcatagg cttggttatg ccggtactgc cgggcctctt 180
gcgggatatc gtccattccg acagcatcgc cagtcactat ggcgtgctgc tagcgctata 240
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71 cacacccgtc ctgtggatcc tctacgccgg acgcatcgtg gccggcatca ccggcgccac    420
73 aggtgcggtt gctggcgcct atatcgccga catcaccgat ggggaagatc gggctcgcca    480
75 cttcgggctc atgagcgctt gtttcggcgt gggtatggtg gcaggccccg tggccggggg    540
77 actgttgggc gccatctcct tgcatgcacc attccttgcg gcggcggtgc tcaacggcct    600
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82 <212> TYPE: PRT
83 <213> ORGANISM: Bacteriophage P1
85 <400> SEQUENCE: 4
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88 1               5                  10                  15
91 Ser Val Ile Gly Gly Ile Gly Thr Phe Leu Met Asp Val Arg Asp Gly
92             20                  25                  30
95 Arg Gln Ser Gly Asn Leu Leu Gly Leu Val Thr Glu Ile Phe Val Ala
96         35                  40                  45
99 Val Thr Ala Gly Ala Val Ala Tyr Leu Leu Gly Gln His Glu Gly Trp
100     50                  55                  60
103 Glu Leu Ser Ile Thr Tyr Leu Met Val Thr Ile Ala Ser Asn Asn Gly
104 65                  70                  75                  80
107 His Glu Val Ile Ser Gly Met Lys Arg Val Asn Ile Asp Ser Ile Leu
108                 85                  90                  95
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112             100                 105
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116 <211> LENGTH: 68
117 <212> TYPE: PRT
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127             20                  25                  30
130 Trp Val Ala Ile Gly Val Leu Gly Ser Leu Leu Phe Gly Leu Leu Thr
131         35                  40                  45
134 Tyr Leu Thr Asn Leu Tyr Phe Lys Ile Arg Glu Asp Arg Arg Lys Ala
135     50                  55                  60
138 Val Arg Gly Glu
139 65
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143 <211> LENGTH: 96
144 <212> TYPE: PRT
145 <213> ORGANISM: Bacteriophage A118
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154             20                  25                  30
157 Leu Val Pro Ser Lys Trp Leu Pro Thr Val Ser Ile Leu Ile Gly Ala
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161 Ile Leu Gly Ala Leu Ala Thr Phe Leu Asp Gly Ser Gly Ser Leu Ala
162     50                  55                  60
165 Thr Met Ile Trp Ala Gly Ala Leu Ala Gly Ala Gly Gly Thr Gly Leu
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169 Phe Glu Gln Phe Thr Asn Arg Ser Lys Lys Tyr Gly Glu Asp Asp Lys
170                 85                  90                  95
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174 <211> LENGTH: 143
175 <212> TYPE: PRT
176 <213> ORGANISM: Lactobacillus casei bacteriophage A2
178 <400> SEQUENCE: 7
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184 Ala Leu Val Pro Ala Ala Leu Leu Val Val Gln Thr Ala Ala Ala Val
185             20                  25                  30
188 Phe Gly Tyr Asn Trp Asp Phe Ala Asn Leu Gly Lys Glu Leu Thr Ala
189         35                  40                  45
192 Val Ile Asn Ala Val Phe Ala Leu Leu Thr Ile Val Gly Val Ala Val
193     50                  55                  60
196 Asp Pro Thr Thr Glu Gly Val Ser Asp Ser Gln Gln Ala Leu Ala Tyr
197 65                  70                  75                  80
200 Pro Ala Leu Ile Thr Thr Lys Ala Ala Lys Ile Lys Ser Leu Glu Asp
201                 85                  90                  95
204 Gln Ile Lys Ala Leu Gln Ala Asp Lys Ala Ala Asp Gln Ala Thr Ser
205             100                 105                 110
208 Ala Ala Ser Glu Val Val Pro Glu Thr Ser Ser Ala Ala Pro Ala Glu
209         115                 120                 125
212 Ser Ala Pro Glu Ser Val Ala Pro Val Ala Ser Glu Glu Val Lys
213     130                 135                 140
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217 <211> LENGTH: 142
218 <212> TYPE: PRT
219 <213> ORGANISM: Lactobacillus bacteriophage phig 1e
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227 Leu Ile Ser Phe Phe Ile Gly Val Ile Val Gln Ala Ile Lys Lys Thr
228             20                  25                  30
231 Gly Lys Val Lys Asn Thr Tyr Leu Pro Phe Ile Ser Met Gly Ile Gly
232         35                  40                  45
235 Ile Leu Ala Gly Leu Ala Ala Val Val Val Thr Lys Asp Thr Asn Tyr
236     50                  55                  60
239 Leu Asn Gly Ala Val Ala Gly Leu Ile Val Gly Ala Ala Thr Ser Gly
240 65                  70                  75                  80
243 Leu Thr Asp Gly Leu Ser Val Gly Thr Ser Ala Val Thr Thr Ala Lys
244                 85                  90                  95
247 Ala Thr Lys Asp Ala Ala Lys Thr Ala Ala Ile Thr Gln Ala Val Leu
248             100                 105                 110
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260 <211> LENGTH: 107
261 <212> TYPE: PRT
262 <213> ORGANISM: Lactobacillus delbrueckii subsp. lactis bacteriophage LL-H
264 <400> SEQUENCE: 9
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267 1               5                   10                  15
270 Ala Leu Ala Val Val Ala Ser Val Tyr Val His Leu Lys Ala Lys Ile
271             20                  25                  30
274 Asp Thr Lys Thr Ala Ala Gly Lys Ala Phe Asp Leu Val Gly Lys Leu
275         35                  40                  45
278 Ala Val Trp Ala Val Asn Glu Ala Glu His Ser Gln Asp Gly Gly Ala
279     50                  55                  60
282 Ala Lys Arg Glu Phe Ala Ala Lys Leu Ile Ser Asp Gln Leu Lys Ala
283 65                  70                  75                  80
286 Lys Gly Ile Thr Gly Ile Asp Glu Lys Met Val Tyr Gly Ala Val Glu
287                 85                  90                  95
290 Thr Ala Trp Lys Glu Ala Ile Glu Asn Val Lys
291             100                 105
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296 <212> TYPE: PRT
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299 <400> SEQUENCE: 10
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305 Leu Ser Leu Ala Leu Glu Phe Ile Asp Thr Gly Thr Leu Lys Pro Ser
306             20                  25                  30
309 Val Arg Lys Arg Ile Ala Val Glu Leu Met Val Leu
310         35                  40
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315 <212> TYPE: PRT
316 <213> ORGANISM: bacteriophage phi AM2
318 <400> SEQUENCE: 11
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321 1               5                   10                  15
324 Thr Ala Leu Pro Ala Leu Ser Val Phe Ile Gly Val Ile Gly Lys Ala
325             20                  25                  30
328 Tyr Gly Trp Gly Gly Thr Asp Leu Ala Ile Ile Thr Leu Asn Ala Phe
329         35                  40                  45
332 Thr Val Phe Leu Gly Thr Leu Ala Gly Val Ser Ala Val Lys Tyr Asn
333     50                  55                  60
336 Ser Gln Pro Asn Asp Thr Lys Glu Asn Lys
337 65                  70
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Input Set : **A:\PTO.FG.txt**
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342 <212> TYPE: PRT
343 <213> ORGANISM: Bacteriophage Tuc2009
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348 1               5                  10                  15
351 Leu Ala Leu Leu Pro Ala Leu Phe Leu Leu Ile Gln Ala Ile Gly Ala
352             20                  25                  30
355 Pro Phe Gly Tyr Lys Trp Asp Phe Val Ile Leu Asn Gln Gln Leu Ala
356         35                  40                  45
359 Ala Val Val Asn Ala Ala Phe Ala Leu Leu Ala Ile Val Gly Val Val
360     50                  55                  60
363 Ala Asp Pro Thr Thr Ser Gly Leu Gly Asp Ser Asp Arg Val Leu Asn
364 65                  70                  75                  80
367 Lys Asp Lys Ser Glu Glu Asn Lys
368                 85
371 <210> SEQ ID NO: 13
372 <211> LENGTH: 88
373 <212> TYPE: PRT
374 <213> ORGANISM: Bacteriophage TPW22
376 <400> SEQUENCE: 13
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383             20                  25                  30
386 Ser Phe Gly Tyr Lys Trp Asn Phe Val Ile Leu Asn Gln Gln Leu Ala
387         35                  40                  45
390 Ala Val Val Asn Ala Ala Phe Ala Leu Leu Ala Ile Val Gly Val Val
391     50                  55                  60
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395 65                  70                  75                  80
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399                 85
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404 <212> TYPE: PRT
405 <213> ORGANISM: Artificial Sequence
407 <220> FEATURE:
408 <223> OTHER INFORMATION: Synthetic Construct
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417             20                  25                  30
420 Ala Ile Phe Gly Ile Leu Phe Gly Leu Phe Thr Met Leu Ile Asn Trp
421         35                  40                  45
424 Tyr Tyr Lys Asn Lys Glu Ile Lys Leu Lys Glu Thr Ala Leu Lys Gln
425     50                  55                  60
```

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